This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

SEQUENCE LISTING

<110> ALTENBUCHNER, JOSEF

MATTES, RALF

PIETZSCH, MARKUS

SYLDATK, CHRISTOPH

WIESE, ANJA

WILMS, BURKARD

<120> RECOMBINANT L-N-CARBAMOYLASE FROM ARTHROBACTER AURESCENS AND METHOD OF PRODUCING L-AMINO ACIDS THEREWITH

<130> RECOMBINANT L-N-CARBAMOYLASE

<140>

<141>

<150> DE 198 14 813.5

<151> 1998-04-02

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 1239

<212> DNA

<213> Arthrobacter aurescens

<400> 1

gtgaccctgc agaaagcgca agcggcgcgc attgagaaag agatccggga gctctccggg 60

ttctcggcag aaggccccgg tgttacccgg ctgacctaca ctccagagca tgccgccgcg 120

cgggaaacgc tcattgcggc tatgaaagcg gccgccttga gcgttcgtga agacgcactc 180

ggaaacatca tcggccgacg tgaaggcact gatccggagc ttcctgcgat cgcggtcggt 240

tcacacttcg attctgtccg aaacggcggg atgtttgatg gcactgcagg cgtggtgtgc 300

gcccttgagg ctgcccgggt gatgctggag aacggctacg tgaatcggca tccatttgag 360

ttcatcgcga tcgtggagga ggaaggggcc cgcttcagca gtggcatgtt gggcggccgg 420

gccattgcag ggttggtcgc cgacagggaa ctggactctt tggttgatga ggatggagtg 480

tccgttaggc aggcggctac tgccttcggc ttgaagccgg gcgaactgca ggctgcagcc 540

cgctccgcgg cggacctgcg tgcttttatc gaactacaca ttgaacaagg accgatcctc 600

gagcaggagc aaatagagat cggagttgta acctccatcg ttggcgttcg cgcattgcgg 660

gttgccgtca aaggcagaag cgaccacgcc ggcacaaccc ccatgcacct gcgccaggat 720

gcgctggtac ccgccgctct catggtgagg gaggtcaacc ggttcgtcaa cgagatcgcc 780

gatggcacag tggctaccgt tggccacctc acagtggccc ccggtggagg caaccaggtc 840

ccgggggagg tggacttcac actggacctg cgttctccgc atgaggagtc gctccgcgtg 900

ctgatcgacc gcatctcggt catggtcggc gaggtcgcct cccaggccgg tgtggctgcc 960

gatgtggatg aatttttcaa tctcagcccg gtgcagctgg ctcctaccat ggtggacgcc 1020

gttcgcgaag cggcctcggc cttgcagttc acacaccggg atatcagcag tggggcgggc 1080

cacgactcga tgttcatcgc ccaggtcacg gacgtcggaa tggttttcgt tccaagccgt 1140

gctggccgga gccacgttcc cgaagaatgg accgatttcg atgaccttcg caaaggaact 1200

gaggttgtcc tccgggtaat gaaggcactt gaccggtaa 1239

<210> 2

<211> 412

<212> PRT

<213> Arthrobacter aurescens

<400> 2

Met Thr Leu Gln Lys Ala Gln Ala Ala Arg Ile Glu Lys Glu Ile Arg
1 5 10 15

Glu Leu Ser Arg Phe Ser Ala Glu Gly Pro Gly Val Thr Arg Leu Thr
20 25 30

Tyr Thr Pro Glu His Ala Ala Ala Arg Glu Thr Leu Ile Ala Ala Met
35 40 45

Lys Ala Ala Ala Leu Ser Val Arg Glu Asp Ala Leu Gly Asn Ile Ile
50 55 60

Gly Arg Arg Glu Gly Thr Asp Pro Glu Leu Pro Ala Ile Ala Val Gly
65 70 75 80

Ser His Phe Asp Ser Val Arg Asn Gly Gly Met Phe Asp Gly Thr Ala
85 90 95

Gly Val Val Cys Ala Leu Glu Ala Ala Arg Val Met Leu Glu Asn Gly
100 105 110

Tyr Val Asn Arg His Pro Phe Glu Phe Ile Ala Ile Val Glu Glu Glu
115 120 125

Gly Ala Arg Phe Ser Ser Gly Met Leu Gly Gly Arg Ala Ile Ala Gly
130 135 140

Leu Val Ala Asp Arg Glu Leu Asp Ser Leu Val Asp Glu Asp Gly Val
145 150 155 160

Ser Val Arg Gln Ala Ala Thr Ala Phe Gly Leu Lys Pro Gly Glu Leu
165 170 175

Gln Ala Ala Ala Arg Ser Ala Ala Asp Leu Arg Ala Phe Ile Glu Leu
180 185 190

His Ile Glu Gln Gly Pro Ile Leu Glu Gln Glu Gln Ile Glu Ile Gly
195 200 205

Val Val Thr Ser Ile Val Gly Val Arg Ala Leu Arg Val Ala Val Lys
210 215 220

Gly Arg Ser Asp His Ala Gly Thr Thr Pro Met His Leu Arg Gln Asp
225 230 235 240

Ala Leu Val Pro Ala Ala Leu Met Val Arg Glu Val Asn Arg Phe Val
245 250 255

Asn Glu Ile Ala Asp Gly Thr Val Ala Thr Val Gly His Leu Thr Val
260 265 270

Ala Pro Gly Gly Gly Asn Gln Val Pro Gly Glu Val Asp Phe Thr Leu
275 280 285

Asp Leu Arg Ser Pro His Glu Glu Ser Leu Arg Val Leu Ile Asp Arg
290 295 300

Ile Ser Val Met Val Gly Glu Val Ala Ser Gln Ala Gly Val Ala Ala
305 310 315 320

Asp Val Asp Glu Phe Phe Asn Leu Ser Pro Val Gln Leu Ala Pro Thr
325 330 335

Met Val Asp Ala Val Arg Glu Ala Ala Ser Ala Leu Gln Phe Thr His
340 345 350

Arg Asp Ile Ser Ser Gly Ala Gly His Asp Ser Met Phe Ile Ala Gln
355 360 365

Val Thr Asp Val Gly Met Val Phe Val Pro Ser Arg Ala Gly Arg Ser
370 375 380

His Val Pro Glu Glu Trp Thr Asp Phe Asp Asp Leu Arg Lys Gly Thr
385 390 395 400

Glu Val Val Leu Arg Val Met Lys Ala Leu Asp Arg
405 410